RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/579,690
Source: TFWP
Date Processed by STIC: 05/31/2006

ENTERED

IFWP

RAW SEQUENCE LISTING DATE: 05/31/2006
PATENT APPLICATION: US/10/579,690 TIME: 13:31:55

Input Set: E:\SEQLIST.txt
Output Set: N:\CRF4\05312006\J579690.raw

```
     4 <110> APPLICANT: BASF AKTIENGESELLSCHAFT et al.
     6 <120> TITLE OF INVENTION: METHODS FOR THE PREPARATION OF LYSINE BY
     7       FERMENTATION OF CORYNEBACTERIUM GLUTAMICUM
    10 <130> FILE REFERENCE: BGI-158PC2
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/579,690
C--> 13 <141> CURRENT FILING DATE: 2006-05-18
    15 <150> PRIOR APPLICATION NUMBER: PCT/IB2003/006456
    16 <151> PRIOR FILING DATE: 2003-12-18
    18 <160> NUMBER OF SEQ ID NOS: 24
    20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
    22 <210> SEQ ID NO: 1
    23 <211> LENGTH: 1070
    24 <212> TYPE: DNA
    25 <213> ORGANISM: Corynebacterium glutamicum
    27 <220> FEATURE:
    28 <221> NAME/KEY: CDS
    29 <222> LOCATION: (22)...(1029)
    31 <400> SEQUENCE: 1
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    33                        Met Asn Leu Lys Asn Pro Glu Thr Pro Asp
    34                         1               5                  10
    36 cgt aac ctt gct atg gag ctg gtg cga gtt acg gaa gca gct gca ctg   99
    37 Arg Asn Leu Ala Met Glu Leu Val Arg Val Thr Glu Ala Ala Ala Leu
    38                 15                  20                  25
    40 gct tct gga cgt tgg gtt gga cgt ggc atg aag aat gaa ggc gac ggt   147
    41 Ala Ser Gly Arg Trp Val Gly Arg Gly Met Lys Asn Glu Gly Asp Gly
    42             30                  35                  40
    44 gcc gct gtt gac gcc atg cgc cag ctc atc aac tca gtg acc atg aag   195
    45 Ala Ala Val Asp Ala Met Arg Gln Leu Ile Asn Ser Val Thr Met Lys
    46         45                  50                  55
    48 ggc gtc gtt gtt atc ggc gag ggc gaa aaa gac gaa gct cca atg ctg   243
    49 Gly Val Val Val Ile Gly Glu Gly Glu Lys Asp Glu Ala Pro Met Leu
    50     60                  65                  70
    52 tac aac ggc gaa gag gtc gga acc ggc ttt gga cct gag gtt gat atc   291
    53 Tyr Asn Gly Glu Glu Val Gly Thr Gly Phe Gly Pro Glu Val Asp Ile
    54 75                  80                  85                  90
    56 gca gtt gac cca gtt gac ggc acc acc ctg atg gct gag ggt cgc ccc   339
    57 Ala Val Asp Pro Val Asp Gly Thr Thr Leu Met Ala Glu Gly Arg Pro
    58                 95                 100                 105
    60 aac gca att tcc att ctc gca gct gca gag cgt ggc acc atg tac gat   387
    61 Asn Ala Ile Ser Ile Leu Ala Ala Ala Glu Arg Gly Thr Met Tyr Asp
    62             110                 115                 120
    64 cca tcc tcc gtc ttc tac atg aag aag atc gcc gtg gga cct gag gcc   435
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65 Pro Ser Ser Val Phe Tyr Met Lys Lys Ile Ala Val Gly Pro Glu Ala
66         125                 130                 135
68 gca ggc aag atc gac atc gaa gct cca gtt gcc cac aac atc aac gcg   483
69 Ala Gly Lys Ile Asp Ile Glu Ala Pro Val Ala His Asn Ile Asn Ala
70     140                 145                 150
72 gtg gca aag tcc aag gga atc aac cct tcc gac gtc acc gtt gtc gtg   531
73 Val Ala Lys Ser Lys Gly Ile Asn Pro Ser Asp Val Thr Val Val Val
74 155                 160                 165                 170
76 ctt gac cgt cct cgc cac atc gaa ctg atc gca gac att cgt cgt gca   579
77 Leu Asp Arg Pro Arg His Ile Glu Leu Ile Ala Asp Ile Arg Arg Ala
78                 175                 180                 185
80 ggc gca aag gtt cgt ctc atc tcc gac ggc gac gtt gca ggt gca gtt   627
81 Gly Ala Lys Val Arg Leu Ile Ser Asp Gly Asp Val Ala Gly Ala Val
82             190                 195                 200
84 gca gca gct cag gat tcc aac tcc gtg gac atc atg atg ggc acc ggc   675
85 Ala Ala Ala Gln Asp Ser Asn Ser Val Asp Ile Met Met Gly Thr Gly
86         205                 210                 215
88 gga acc cca gaa ggc atc atc act gcg tgc gcc atg aag tgc atg ggt   723
89 Gly Thr Pro Glu Gly Ile Ile Thr Ala Cys Ala Met Lys Cys Met Gly
90     220                 225                 230
92 ggc gaa atc cag ggc atc ctg gcc cca atg aac gat ttc gag cgc cag   771
93 Gly Glu Ile Gln Gly Ile Leu Ala Pro Met Asn Asp Phe Glu Arg Gln
94 235                 240                 245                 250
96 aag gca cac gac gct ggt ctg gtt ctt gat cag gtt ctg cac acc aac   819
97 Lys Ala His Asp Ala Gly Leu Val Leu Asp Gln Val Leu His Thr Asn
98                 255                 260                 265
100 gat ctg gtg agc tcc gac aac tgc tac ttc gtg gca acc ggt gtg acc   867
101 Asp Leu Val Ser Ser Asp Asn Cys Tyr Phe Val Ala Thr Gly Val Thr
102             270                 275                 280
104 aac ggt gac atg ctc cgt ggc gtt tcc tac cgc gca aac ggc gca acc   915
105 Asn Gly Asp Met Leu Arg Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr
106         285                 290                 295
108 acc cgt tcc ctg gtt atg cgc gca aag tca ggc acc atc cgc cac atc   963
109 Thr Arg Ser Leu Val Met Arg Ala Lys Ser Gly Thr Ile Arg His Ile
110     300                 305                 310
112 gag tct gtc cac cag ctg tcc aag ctg cag gaa tac tcc gtg gtt gac   1011
113 Glu Ser Val His Gln Leu Ser Lys Leu Gln Glu Tyr Ser Val Val Asp
114 315                 320                 325                 330
116 tac acc acc gcg acc taa gagctcttag ttcgaaaaac cgccggccat          1059
117 Tyr Thr Thr Ala Thr  *
118                 335
120 tgtggtcggc g                                                     1070
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 335
124 <212> TYPE: PRT
125 <213> ORGANISM: Corynebacterium glutamicum
127 <400> SEQUENCE: 2
128 Met Asn Leu Lys Asn Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu
129  1               5                  10                  15
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130 Leu Val Arg Val Thr Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val
131             20                  25                  30
132 Gly Arg Gly Met Lys Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met
133         35                  40                  45
134 Arg Gln Leu Ile Asn Ser Val Thr Met Lys Gly Val Val Val Ile Gly
135     50                  55                  60
136 Glu Gly Glu Lys Asp Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val
137 65                  70                  75                  80
138 Gly Thr Gly Phe Gly Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp
139                 85                  90                  95
140 Gly Thr Thr Leu Met Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu
141             100                 105                 110
142 Ala Ala Ala Glu Arg Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr
143         115                 120                 125
144 Met Lys Lys Ile Ala Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile
145     130                 135                 140
146 Glu Ala Pro Val Ala His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly
147 145                 150                 155                 160
148 Ile Asn Pro Ser Asp Val Thr Val Val Val Leu Asp Arg Pro Arg His
149                 165                 170                 175
150 Ile Glu Leu Ile Ala Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu
151             180                 185                 190
152 Ile Ser Asp Gly Asp Val Ala Gly Ala Val Ala Ala Ala Gln Asp Ser
153         195                 200                 205
154 Asn Ser Val Asp Ile Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile
155     210                 215                 220
156 Ile Thr Ala Cys Ala Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile
157 225                 230                 235                 240
158 Leu Ala Pro Met Asn Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly
159                 245                 250                 255
160 Leu Val Leu Asp Gln Val Leu His Thr Asn Asp Leu Val Ser Ser Asp
161             260                 265                 270
162 Asn Cys Tyr Phe Val Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg
163         275                 280                 285
164 Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met
165     290                 295                 300
166 Arg Ala Lys Ser Gly Thr Ile Arg His Ile Glu Ser Val His Gln Leu
167 305                 310                 315                 320
168 Ser Lys Leu Gln Glu Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
169                 325                 330                 335
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 35
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Synthetic construct
180 <400> SEQUENCE: 3
181 gagagagaga cgcgtcccag tggctgagac gcatc                              35
183 <210> SEQ ID NO: 4
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Input Set : **E:\SEQLIST.txt**
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<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic construct
<400> SEQUENCE: 4
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<210> SEQ ID NO: 5
<211> LENGTH: 4323
<212> TYPE: DNA
<213> ORGANISM: Corynebacterium glutamicum
<400> SEQUENCE: 5
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ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtggtttt 2220

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237 tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc 2280
238 ttttctacgg ggtctgacgc tcagtggaac gaaaactcac gttaagggat tttggtcatg 2340
239 agattatcaa aaaggatctt cacctagatc cttttaaagg ccggccgcgg ccgccatcgg 2400
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250 ttgttaaata aagattcttc gccttggtag ccatcttcag ttccagtgtt tgcttcaaat 3060
251 actaagtatt tgtggccttt atcttctacg tagtgaggat ctctcagcgt atggttgtcg 3120
252 cctgagctgt agttgccttc atcgatgaac tgctgtacat tttgatacgt ttttccgtca 3180
253 ccgtcaaaga ttgatttata atcctctaca ccgttgatgt tcaaagagct gtctgatgct 3240
254 gatacgttaa cttgtgcagt tgtcagtgtt tgtttgccgt aatgtttacc ggagaaatca 3300
255 gtgtagaata aaaggatttt tcagtcagat gtaaatgtgg ctgaacctga ccatctttgt 3360
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257 ccagcgtttt tccagctgtc aatagaagtt tcgccgactt tttgatagaa catgtaaatc 3480
258 gatgtgtcat ccgcattttt aggatctccg gctaatgcaa agacgatgtg gtagccgtga 3540
259 tagtttgcga cagtgccgtc agcgttttgt aatggccagc tgtcccaaac gtccaggcct 3600
260 tttgcagaag agatattttt aattgtggac gaatcaaatt cagaaacttg atatttttca 3660
261 ttttttgct gttcagggat ttgcagcata tcatggcgtg taatatggga aatgccgtat 3720
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263 agcagtgcgg tagtaaaggt taatactgtt gcttgttttg caaacttttt gatgttcatc 3840
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265 gaagatggca agttagttac gcacaataaa aaaagaccta aaatatgtaa ggggtgacgc 3960
266 caaagtatac actttgccct ttacacattt taggtcttgc ctgctttatc agtaacaaac 4020
267 ccgcgcgatt tacttttcga cctcattcta ttagactctc gtttggattg caactggtct 4080
268 attttcctct tttgtttgat agaaaatcat aaaaggattt gcagactacg ggcctaaaga 4140
269 actaaaaaat ctatctgttt cttttcattc tctgtatttt ttatagtttc tgttgcatgg 4200
270 gcataaagtt gccttttttaa tcacaattca gaaaatatca taatatctca tttcactaaa 4260
271 taatagtgaa cggcaggtat atgtgatggg ttaaaaagga tcggcggccg ctcgatttaa 4320
272 atc 4323
274 <210> SEQ ID NO: 6
275 <211> LENGTH: 5860
276 <212> TYPE: DNA
277 <213> ORGANISM: Corynebacterium glutamicum
279 <400> SEQUENCE: 6
280 cccggtacca cgcgtcccag tggctgagac gcatccgcta aagccccagg aaccctgtgc 60
281 agaaagaaaa cactcctctg gctaggtaga cacagtttat aaaggtagag ttgagcgggt 120
282 aactgtcagc acgtagatcg aaaggtgcac aaaggtggcc ctggtcgtac agaaatatgg 180
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284 caagaaggct ggaaatgatg tcgtggttgt ctgctccgca atgggagaca ccacggatga 300
285 acttctagaa cttgcagcgg cagtgaatcc cgttccgcca gctcgtgaaa tggatatgct 360
286 cctgactgct ggtgagcgta tttctaacgc tctcgtcgcc atggctattg agtcccttgg 420
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VERIFICATION SUMMARY DATE: 05/31/2006
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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date